

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:58:49 ; Search time 29 Seconds  
(without alignments)  
106.576 Million cell updates/sec

Title: US-09-300-612-1

Perfect score: 84

Sequence: 1 LKAMDPTPLWKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	17	6	Q9TR78
2	46	54.8	729	5	Q9VQP3
3	46	54.8	856	5	Q9GZ10
4	46	54.8	1219	5	Q9VT64
5	46	54.8	1221	5	Q8SZR7
6	45	53.6	97	12	Q91P83
7	45	53.6	97	12	Q91ME9
8	45	53.6	312	6	Q9N126
9	44	52.4	125	4	Q9NV61
10	44	52.4	377	16	Q9T232
11	44	52.4	695	17	Q9UZG1
12	44	52.4	1327	4	O15070
13	43	51.2	278	10	Q946H8
14	43	51.2	354	2	Q8VM74
15	43	51.2	406	10	Q944S7
16	43	51.2	687	10	Q9LMT8

17	42	50.0	97	12	Q920B3
18	42	50.0	115	17	O59492
19	42	50.0	240	2	Q9RC28
20	42	50.0	457	10	O22618
21	42	50.0	580	4	Q9UJ46
22	42	50.0	621	10	Q94JH4
23	42	50.0	809	4	Q9BW82
24	42	50.0	840	4	Q9UJ45
25	42	50.0	853	4	Q9UJ47
26	42	50.0	923	11	Q91X64
27	42	50.0	1322	5	Q9NJS5
28	42	50.0	1322	5	Q9NAT0
29	41.5	49.4	693	16	Q9K437
30	41	48.8	165	5	Q9W3H5
31	41	48.8	194	4	Q9NWD3
32	41	48.8	222	4	Q9HB78
33	41	48.8	222	10	Q8SQ02
34	41	48.8	290	2	Q8V046
35	41	48.8	349	11	O5S087
36	41	48.8	411	16	O8YTE5
37	41	48.8	498	11	Q9CSL7
38	41	48.8	505	2	Q9R9S3
39	41	48.8	707	16	Q9CD82
40	41	48.8	792	11	O8VDM3
41	41	48.8	961	16	Q8XF26
42	41	48.8	967	2	O54123
43	41	48.8	975	2	O30354
44	41	48.8	1259	4	Q8WXX7
45	41	48.8	1559	10	O49889

## ALIGNMENTS

RESULT 1

Q9TR78 ID Q9TR78 PRELIMINARY; PRT; 17 AA.  
AC Q9TR78  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE ANTI-BOTHRIC complex 48,000 SUBUNIT (Fragment).  
OS Didelphis marsupialis (Southern opossum).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.  
OX NCBI\_TaxID=9268;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95149299; PubMed=7846694;  
RA Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.;  
RT "Isolation and partial characterization of an anti-bothropic complex  
from the serum of South American Didelphidae.";  
RL Toxicon 32:1237-1249(1994).  
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match

Best Local Similarity 100.0%; Score 84; DB 6; Length 17;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWKTE 15

|||||

1 LKAMDPTPLWKTE 15

RESULT 2

Q9VQP3 ID Q9VQP3 PRELIMINARY; PRT; 729 AA.

AC Q9VQP3

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE CG3327 protein.

GN E23 OR CG3327.

OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT The genome sequence of Drosophila melanogaster.  
 RL Science 287:2185-2195(2000).  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.  
 DR EMBL: AE003580; AAF51122.1;  
 DR FlyBase: FBgn002045; E23.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR Pfam: PF00005; ABC\_tran; 1.  
 DR ProDom: PD000006; ABC\_transportr; 1.  
 DR SMART: SM00382; AAA; 1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER; 1.  
 KW ATP-binding; Transport.  
 SQ SEQUENCE 729 AA; 82879 MW; E5D925787009069C CRC64;  
 Query Match 54.8%; Score 46; DB 5; Length 729;  
 Best Local Similarity 57.1%; Pred. No. 39;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LKAMDPTPLMIKT 14  
 DB 689 LKAQNSTPLMIKT 702  
 RESULT 3  
 Q9GZ10  
 ID Q9GZ10  
 AC Q9GZ10  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21; Last annotation update)  
 DE E23.  
 GN E23 OR CG3327.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20402567; PubMed=10931948;  
 RX Hock T., Cottrill T., Keegan J., Garza D.;  
 RT "The E23 early gene of Drosophila encodes an ecdysone-inducible ATP-  
 RT binding cassette transporter capable of repressing ecdysone-mediated  
 RL gene activation."  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9519-9524(2000).  
 DR EMBL: AF270979; AAG02041.1;  
 DR FlyBase: FBgn002045; E23.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003439; ABC\_transportr.  
 DR Pfam: PF00005; ABC\_tran; 1.  
 DR ProDom: PD000006; ABC\_transportr; 1.  
 DR SMART: SM00382; AAA; 1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER; UNKNOWN\_1.  
 KW ATP-binding.  
 SQ SEQUENCE 856 AA; 95080 MW; BAAE8964A5D806D6 CRC64;  
 Query Match 54.8%; Score 46; DB 5; Length 856;  
 Best Local Similarity 57.1%; Pred. No. 46;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LKAMDPTPLMIKT 14  
 DB 816 LKAQNSTPLMIKT 829  
 RESULT 4  
 Q9VT64  
 ID Q9VT64 PRELIMINARY; PRT; 1219 AA.  
 AC Q9VT64  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE TAF150 protein.  
 GN TAF150 OR CG6711.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 FT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003550; AAF50190.1;  
 DR FlyBase: FBgn0011836; tafi50.  
 DR InterPro: IPR001930; Ala\_peptase.  
 DR InterPro: IPR002052; N6\_Mtase.  
 DR Pfam: PF01433; Peptidase\_M1; 1.  
 DR PROSITE: PS00092; N6\_MTASE; UNKNOWN.1.  
 SQ SEQUENCE 1219 AA; 139210 MW; 964683361C47D105 CRC64;

Query Match 54.8%; Score 46; DB 5; Length 1219;  
 Best Local Similarity 53.3%; Pred. No. 66;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15  
 ||||:||||:  
 Db 618 LSAMDSPVLWRLD 632

RESULT 5  
 Q8SZR7 PRELIMINARY; PRT; 1221 AA.  
 AC Q8SZR7;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DE LD43729p.  
 DE "Direct submission."  
 GN TAF150.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY070564; AAL48035.1;  
 SQ SEQUENCE 1221 AA; 139498 MW; C2DC066826B1AF6E CRC64;

Query Match 54.8%; Score 46; DB 5; Length 1221;  
 Best Local Similarity 53.3%; Pred. No. 67;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15  
 ||||:||||:  
 Db 620 LSAMDSPVLWRLD 634

RESULT 6  
 Q91P83 PRELIMINARY; PRT; 97 AA.  
 AC Q91P83;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Vietnam tomato leaf curl geminivirus DNA A, complete  
 DE sequence.  
 GN C4.  
 OS tomato leaf curl virus.  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OX NCBI\_TaxID=28350;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tsai W.S., Hong L.T.A., Green S.K.;  
 RT "Completed sequence of Vietnam tomato leaf curl geminivirus.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF264063; AAK58531.1;  
 DR InterPro: IPR002488; Geminl\_C4.  
 DR Pfam: PF01492; Geminl\_C4; 1.  
 SQ SEQUENCE 97 AA; 11153 MW; D8761816CD5F94AD CRC64;

Query Match 53.6%; Score 45; DB 12; Length 97;  
 Best Local Similarity 53.3%; Pred. No. 7;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15  
 ||||:||||:  
 Db 42 LKAQMSKPIWTKTE 56

RESULT 7  
 Q91ME9 PRELIMINARY; PRT; 97 AA.  
 AC Q91ME9;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE C4 protein.  
 GN C4.  
 OS pepper leaf curl virus.  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OX NCBI\_TaxID=83839;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shih S.L., Green S.K., Ahmad I., Smith J.;  
 RT "Direct submission."  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF336806; AAK69638.1;  
 DR InterPro: IPR002488; Geminl\_C4.  
 DR Pfam: PF01492; Geminl\_C4; 1.  
 SQ SEQUENCE 97 AA; 10965 MW; FCB6775D884266CA CRC64;

Query Match 53.6%; Score 45; DB 12; Length 97;  
 Best Local Similarity 53.3%; Pred. No. 7;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15  
 ||||:||||:  
 Db 42 LKALQMSKPMWRKTE 56

RESULT 8  
 Q9N126 PRELIMINARY; PRT; 312 AA.  
 ID Q9N126;  
 AC Q9N126;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Photoreceptor outer segment all-trans retinol dehydrogenase.  
 GN PRRDH.  
 OS Bos taurus (Bovine).

DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20219146; PubMed=10753906;  
 RA Ratner A., Smallwood P.M., Nathans J.;  
 RT "Identification and characterization of all-trans-retinol  
 dehydrogenase from photoreceptor outer segments, the visual cycle  
 enzyme that reduces all-trans-retinal to all-trans-retinol.";  
 RL J. Biol. Chem. 275:11034-11043(2000).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR EMBL: AF229846; AAF63161.1; -.  
 DR HSSP: P14061; 1FDS.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
 KW Oxidoreductase; Receptor.  
 SQ SEQUENCE 312 AA; 33956 MW; 36481039FF71874D CRC64;

Query Match 53.6%; Score 45; DB 6; Length 312;  
 Best Local Similarity 57.1%; Pred. NO. 24;  
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKT 14  
 ||||| : : : :  
 DB 268 LKAMDPSGLVVRT 281

## RESULT 9

Q9NV61 PRELIMINARY; PRT; 125 AA.  
 ID Q9NV61  
 AC Q9NV61  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE OVARC100060 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OVARIAN CARCINOMA;  
 RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,  
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,  
 RA Masuho Y., Kanehori K.;  
 RT "NEO human cDNA sequencing project.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK001769; BAA91896.1; -.  
 SQ SEQUENCE 125 AA; 13504 MW; F2D324918E3A70B1 CRC64;

Query Match 52.4%; Score 44; DB 4; Length 125;  
 Best Local Similarity 46.2%; Pred. NO. 13;  
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPLWIKT 14  
 | : | : | : | :  
 DB 4 KSMGAPPWRMRS 16

## RESULT 10

Q92T32 PRELIMINARY; PRT; 377 AA.  
 ID Q92T32  
 AC Q92T32  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Putative permease ABC transporter protein.  
 GN R00154 OR SMC02830.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OC NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Gostard T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
 RA Pohl T., Portetelle D., Puchler A., Purnelle B., Rampsperger U.,  
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 Sinorhizobium meliloti strain 1021.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL: AL591782; CAC41541.1; -.  
 DR InterPro: IPR000515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 377 AA; 41867 MW; D8E34131C7E14415 CRC64;

Query Match 52.4%; Score 44; DB 16; Length 377;  
 Best Local Similarity 60.0%; Pred. NO. 41;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTPPLWIKTE 15  
 ||||| : : : :  
 DB 125 PTPPFWLWSE 134

## RESULT 11

Q9UZG1 PRELIMINARY; PRT; 695 AA.  
 ID Q9UZG1  
 AC Q9UZG1  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Hypothetical protein PAB1590.  
 GN PAB1590.  
 OS Pyrococcus abyssii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OC NCBI\_TaxID=29292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ORSAY;  
 RA Heilig R.;  
 RT "Pyrococcus abyssii genome sequence: insights into archaeal chromosome  
 structure and evolution.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ248286; CAB50098.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 695 AA; 79999 MW; 371E0E402210F551 CRC64;

Query Match 52.4%; Score 44; DB 17; Length 695;  
 Best Local Similarity 54.5%; Pred. NO. 78;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPLWIK 13  
 | : | : | : | :  
 DB 561 ANDPKPPWLE 571

## RESULT 12

Q15070 PRELIMINARY; PRT; 1327 AA.  
 ID Q15070  
 AC Q15070  
 DT 01-JAN-1998 (TRENBLrel. 05, Created)  
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE KIAA0364 protein.  
 GN KIAA0364.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=97349984; PubMed=9205841;  
 RA Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,  
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. VII.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 4:141-150(1997).  
 DR EMBL; AB002362; BAA20819.1;  
 DR HSSP; P43626; INKR.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR003600; Ig\_like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 11.  
 DR SMART; SM00408; IGC2; 1.  
 DR SMART; SM00410; IG\_like; 7.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 1327 AA; 147972 MW; 736C689FEC94D2E1 CRC64;

Query Match 52.4%; Score 44; DB 4; Length 1327;  
 Best Local Similarity 63.6%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 MDTPPLWIKT 14  
 |||||  
 DB 25 MDQPELWIES 35

RESULT 13  
 O946H8 PRELIMINARY; PRT; 278 AA.  
 ID O946H8  
 AC O946H8  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Alpha-expansin.  
 GN EXP24.  
 OS Eryka sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21521099; PubMed=11641069;  
 RA Lee Y., Choi D., Kende H.;  
 RT "Expansins: ever-expanding numbers and functions."  
 RL Curr. Opin. Plant Biol. 4:527-532(2001).  
 DR EMBL; AF394559; AAL24495.1;  
 DR InterPro; IPR000882; Pollen\_allergen.  
 DR Pfam; PF01357; Pollen\_allergen; 1.  
 DR ProDom; PD002179; Pollen\_allergen; 1.  
 SQ SEQUENCE 278 AA; 30046 MW; D78E729F091766F0 CRC64;

Query Match 51.2%; Score 43; DB 10; Length 278;  
 Best Local Similarity 66.7%; Pred. No. 44;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 DTPPLWIK 13  
 |||||  
 DB 44 DETPPVWLK 52

RESULT 14  
 O8VM74

ID O8VM74 PRELIMINARY; PRT; 354 AA.  
 AC O8VM74;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative LuxA.  
 OS Rhizobium sp. (strain BR816).  
 OC Plasmid pSymb.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=48291;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR816;  
 RA Luyten E., Verreth C., Vanderleyden J.;  
 RT "Conservation of short-chain alcohol dehydrogenase in rhizobial spp."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR816;  
 RA Luyten E., Swinnen E., Verreth C., Vlassak K., Dombrecht B.,  
 RA Vanderleyden J.;  
 RT "Functional and structural analysis of a P450 homolog gene identified  
 RT in Rhizobium sp. BR816."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U28451; AAL61964.1;  
 DR InterPro; IPR002103; Bac\_luciferase.  
 DR Pfam; PF00295; bac\_luciferase; 1.  
 KW Plasmid.  
 SQ SEQUENCE 354 AA; 39367 MW; 9D18A3F09BA70A42 CRC64;

Query Match 51.2%; Score 43; DB 2; Length 354;  
 Best Local Similarity 85.7%; Pred. No. 56;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTPPLWI 12  
 |||||  
 DB 167 PTPPIWI 173

RESULT 15  
 O944S7 PRELIMINARY; PRT; 406 AA.  
 ID O944S7  
 AC O944S7;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Atlg17920/F2h15.22.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,  
 RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,  
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,  
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RT "Arabidopsis cDNA clones";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF424554; AAL11548.1;  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR002913; START.  
 DR Pfam; PF00046; homeobox; 1.  
 DR Pfam; PF01852; START; 1.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; UNKNOWN\_1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.

SQ SEQUENCE 406 AA; 45986 MW; 045B92F725BD785C CRC64;  
 Query Match 51.2%; Score 43; DB 10; Length 406;  
 Best Local Similarity 46.7%; Pred. No. 65;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKANDPTPLWIKTE 15  
 I : : | : : : :  
 Db 225 LRLQTNPLWIKTD 239

Search completed: June 27, 2003, 18:02:00  
 Job time : 31 secs